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sample and being configured to at least partially resolve at least one component of a said biological sample;

resolving the at least one component of the biological sample to provide thereby an enriched fraction; and

determining a biological sample component expression pattern for the biological sample using the enriched fraction.

Subj B1

2. The method of claim 1, wherein the biological sample components comprise proteins.
3. The method of claim 1, wherein the biological sample components comprise nucleotides.
4. The method of claim 1, wherein said hydrophilic ligand comprises:
a peptoid backbone; and
a plurality of affinity property groups and hydrophilic groups being pendent from said peptoid backbone.
5. The method of claim 4, wherein said hydrophilic groups are intercalated with said affinity property groups.
6. The method of claim 5, wherein said hydrophilic groups alternate with said affinity property groups along said peptoid backbone.
7. The method of claim 6, wherein said affinity property groups are selected from the group consisting of alkyl, (cycloalkyl)alkyl, (cycloheteroalkyl)alkyl, aralkyl, and heteroaralkyl, each substituted optionally from the group consisting of oxo, thia, halo, amino, hydroxy, cyano, nitro, thio, aminocarbonyl, carboxy, and imino.
8. The method of claim 7, wherein said affinity property groups are selected from the group consisting of methyl, hydroxymethyl, prop-2-yl, 2-methylpropyl, pyrrolidylmethyl, methylthioethyl, 1-hydroxyethyl, thiomethyl, aminocarbonylmethyl, aminocarbonylethyl, carboxymethyl, carboxyethyl, 4-aminobutyl, and 3-guanidinopropyl, guanidinoaryl, hydroxyaryl, amidoalkyl, phosphoryl alkyl, phosphoryl aryl, oligoether, and polyhydroxyalkyl.
9. The method of claim 7, wherein said affinity property groups are selected from the group consisting of optionally substituted aralkyl and heteroaralkyl.
10. The method of claim 9, wherein said affinity property groups are selected from the group consisting of phenylmethyl, hydroxyphenylmethyl, imidazolylmethyl, purinylmethyl, pyrimidinylmethyl, and indolylmethyl.

11. The method of claim 7, wherein said affinity groups are selected from the group consisting of optionally substituted amonioalkyl, trialkylamonioalkyl.

12. The method of claim 7, wherein said affinity property groups are optionally substituted carboxylatoalkyl.

13. The method of claim 4, wherein said hydrophilic groups are selected from the group consisting of alkyloxyalkylenyl, aminoalkyl, alkylaminoalkyl, quaternary ammoniumalkyl, hydroxyalkyl, thioalkyl, alkylthioalkylenyl, carboxyalkyl, alkyloxycarbonylalkyl, and aminocarbonylalkyl.

14. The method of claim 13, wherein said hydrophilic group is alkyloxyalkyl.

15. The method of claim 14, wherein said hydrophilic group is selected from the group consisting of methoxyethyl, hydroxyethyl, 1-hydroxyethyl-2-hydroxyethyl, and 2,3-dihydroxypropyl.

16. The method of claim 4, wherein about 50% of said pendant groups are affinity property groups.

17. The method of claim 16, wherein about 33% of said pendant affinity property groups have a common affinity property.

18. The method of claim 16, wherein about 67% of said pendant affinity property groups have a common affinity property.

19. The method of claim 16, wherein about 100% of said pendant affinity property groups have a common affinity property.

20. The method of claim 4, wherein said affinity property groups and said hydrophilic groups are pendant from nitrogen atoms in the backbone.

21. The method of claim 4, wherein said biological sample is derived from a homogeneous source.

22. The method of claim 21, wherein said homogeneous source is a cell line.

23. The method of claim 4, wherein said biological sample is derived from a heterogeneous source.

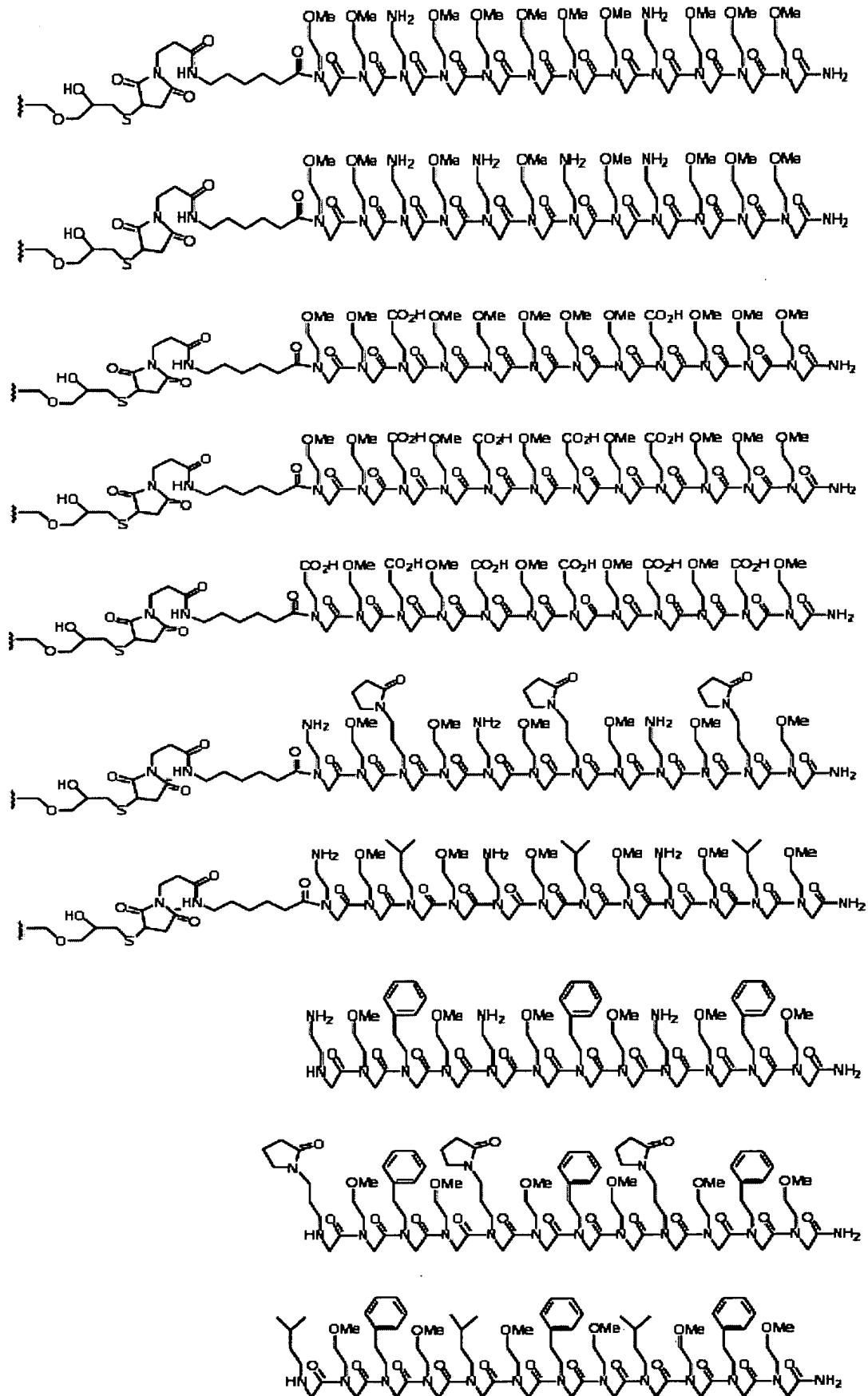
24. The method of claim 23, wherein said heterogeneous source is one or more tissue samples.

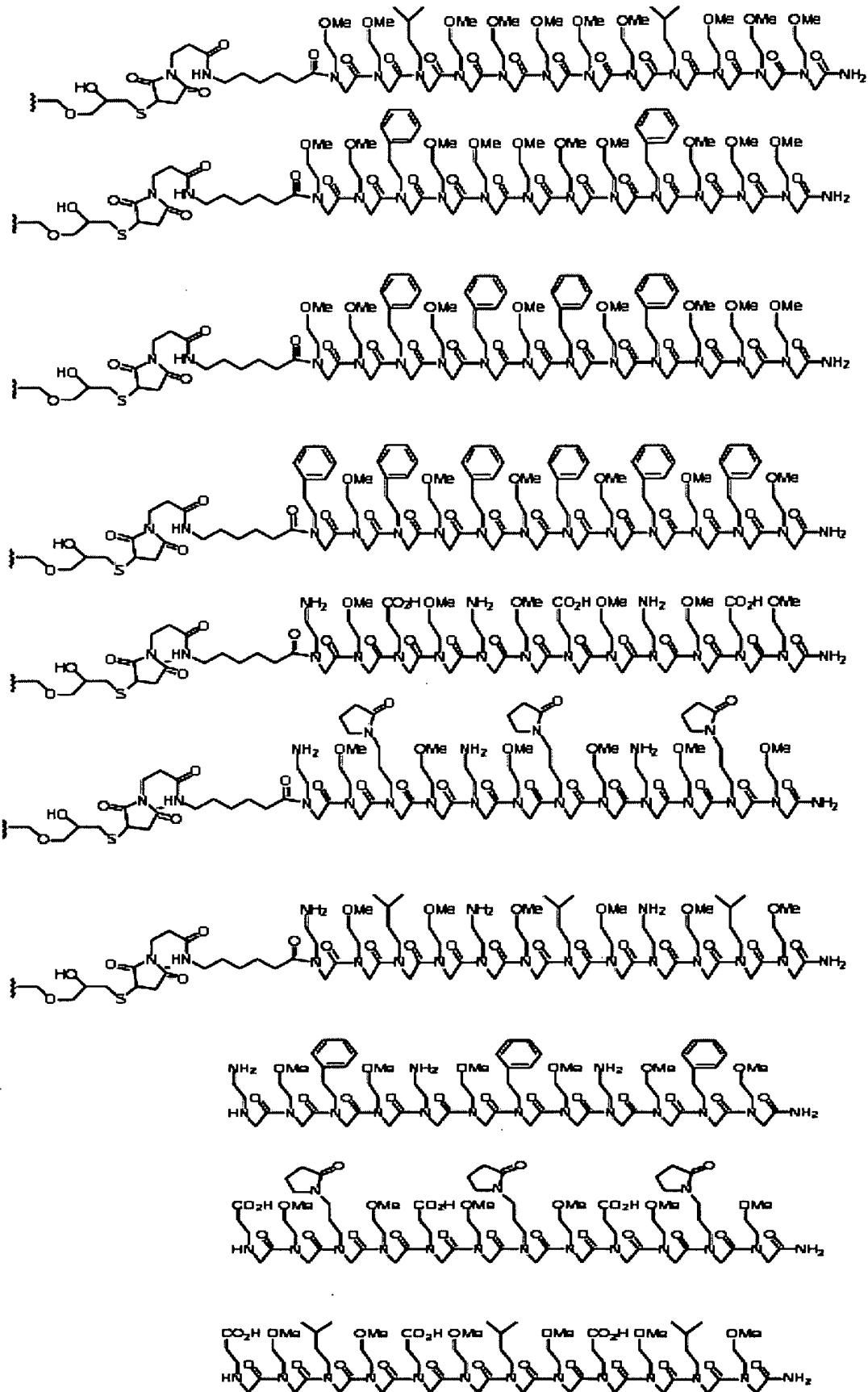
Amend
25. The method of claim 23, wherein said heterogeneous source is one or more blood samples.

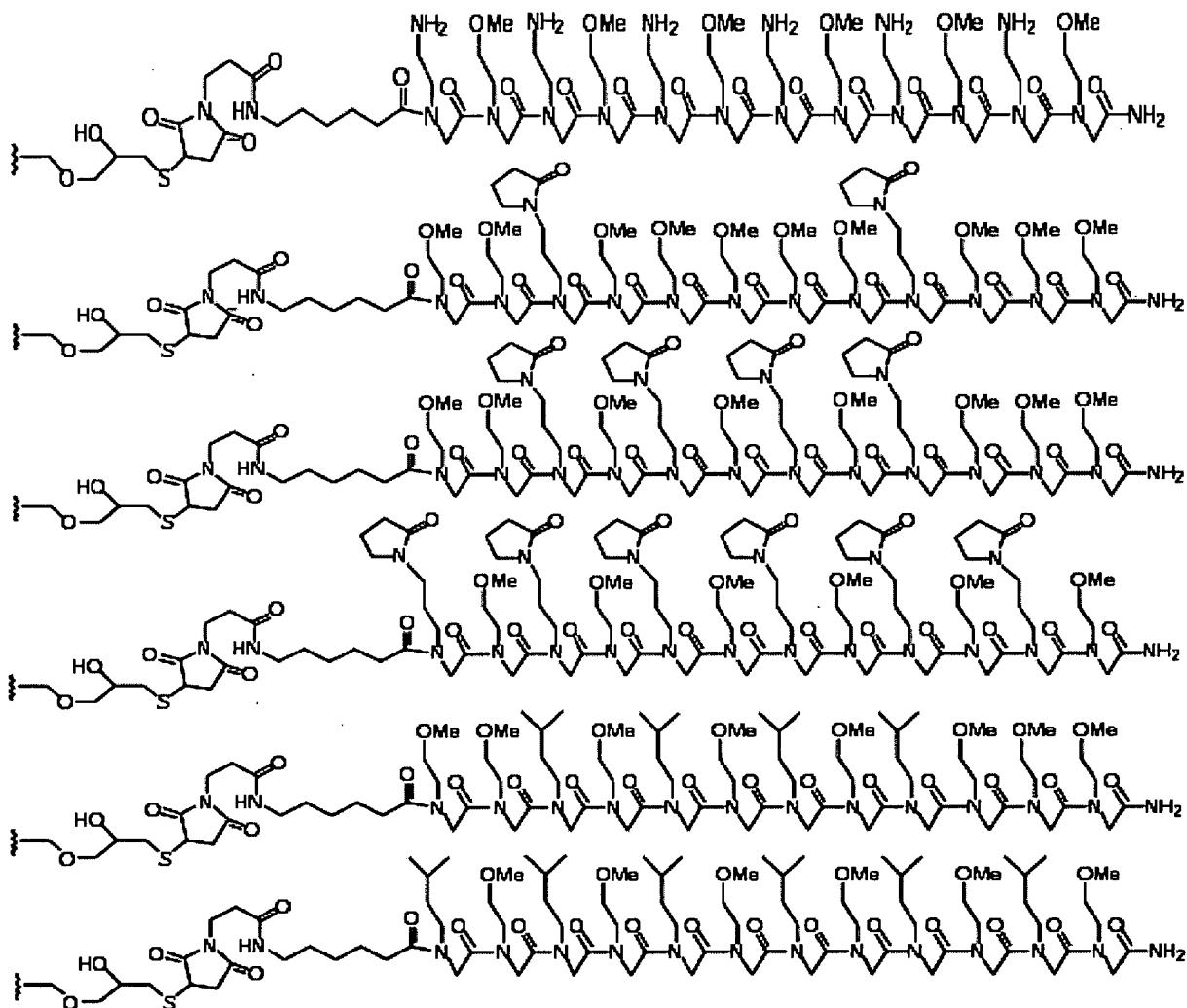
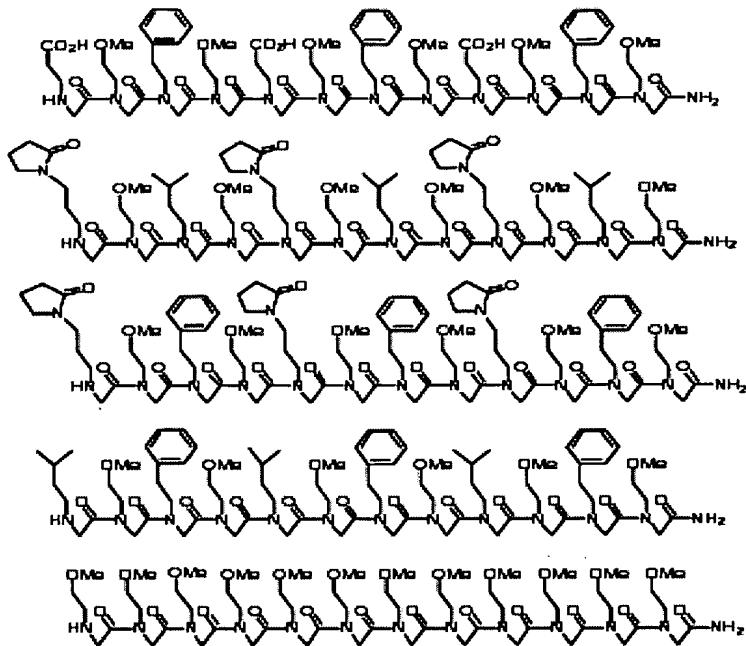
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74. The method of claim 1, wherein the intermediate binding affinity is characterized by the ligand interacting with the components of the biological sample by a combination of non-specific molecular forces consisting essentially of ionic, van der Waal's and hydrogen bond interactions.

75. The method of claim 4, wherein the ligand is selected from the group consisting of the following:

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